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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

## (i) APPLICANT:

- (A) NAME: ZENECA LIMITED  
(B) STREET: 15 STANHOPE GATE  
(C) CITY: LONDON  
(E) COUNTRY: UNITED KINGDOM  
(F) POSTAL CODE (ZIP): W1Y 6LN  
(G) TELEPHONE: 0171 304 5000  
(H) TELEFAX: 0171 304 5151  
(I) TELEX: 0171 834 2042

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## (ii) TITLE OF INVENTION: PROTEINS

## (iii) NUMBER OF SEQUENCES: 131

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

25

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

## (ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGAAGCTTGA AGATGGATAC AGTTGGTGCA GC

32

5 (2) INFORMATION FOR SEQ ID NO: 2:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGAAGCTTAG ACAGATGGGG GTGTCGTTTT G

31

25 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

30

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala  
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
20 25 30

Tyr Met

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GACATTCAGC TGACCCAGTC TCCA

24

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GACATTGAGC TCACCCAGTC TCCA

24

5 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

20 AGGTSMARCT GCAGSAGTCW GG

22

(2) INFORMATION FOR SEQ ID NO: 7:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ACTAGTGGAA TTCAGTGTGA GGTSCARCTG CAGCARTCWG G

41

5 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

20 GACATTGAGC TCACCCAGTC TCCAGCAATC ATGTCTGCAT CTCCAGGGGA GAAGGTCACC 60

ATAACCTGCA GTGCCAGCTC AAGTGTAAC TACATGCACT GGTTCAGCA GAAGCCAGGC 120

ACTTCTCCCA AACTCTGGAT TTATAGCACA TCCAACCTGG CTTCTGGAGT CCCTGCTCGC 180

25

TTCAGTGGCA GTGGATCTGG GACCTCTTAC TCTCTCACA TCAGCCGAAT GGAGGCTGAA 240

GATGCTGCCA CTTATTACTG CCAGCAAAGG AGTACTTACC CGCTCACGTT CGGTGCTGGG 300

30 ACCAAGCTGG AGCTGAAACG GGCTGATGCT GCACCAACTG TATCCATCTT CAAGCTT 357

(2) INFORMATION FOR SEQ ID NO: 9:

35

F00220"0500T060

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly  
 1 5 10 15

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met  
 20 25 30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr  
 35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu  
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr  
 85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala  
 100 105

## 35 (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs

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- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAGGTGCAGC TGCAGCARTC WGGGGCAGAG CTTGTGAGGT CAGGGGCCTC AGTCAAGTTG 60  
TCCTGCACAG CTTCTGGCTT CAACATTAAA GACAACTATA TGCACTGGGT GAAGCAGAGG 120  
CCTGAACAGG GCCTGGAGTG GATTGCATGG ATTGATCCTG AGAATGGTGA TACTGAATAT 180  
GCCCCGAAGT TCCGGGGCAA GGCCACTTTG ACTGCAGACT CATCCTCCAA CACAGCCTAC 240  
CTGCACCTCA GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTACTGTCA TGTCTTGATC 300  
TATGCTGGTT ATTTGGCTAT GGACTACTGG GGTCAAGGAA CCTCAGTCGC CGTCTCCTCA 360

25 (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Ala  
 1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
 20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile  
 35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
 50 55 60

Arg Gly Lys Ala Thr Leu Thr Ala Asp Ser Ser Ser Asn Thr Ala Tyr  
 65 70 75 80

Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Ser Val Ala Val Ser Ser  
 115 120

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AAGCTTTCCC GCGGGGACAT TGAGCTCACC CAGTCTCCA

39

5 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

20 AAGCTTCTCG AGCTTGGTCC CAGCACCGAA

30

(2) INFORMATION FOR SEQ ID NO: 14:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AAGCTTGGAA TTCAGTGTGA GGTGCAGCTG CAGCAG

36

5 (2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

20 AAGCTTCGAG CTCACGGCGA CTGAGGTTCC TTG

33

(2) INFORMATION FOR SEQ ID NO: 16:

(1) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (11) MOLECULE TYPE: other nucleic acid

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60  
5 CGCGGGGACA TTGAGCTCAC CCAGTCTCCA GCAATCATGT CTGCATCTCC AGGGGAGAAG 120  
GTCACCATAA CCTGCAGTGC CAGCTCAAGT GTAACCTACA TGCACTGGTT CCAGCAGAAG 180  
CCAGGCACTT CTCCCAAACCT CTGGATTTAT AGCACATCCA ACCTGGCTTC TGGAGTCCCT 240  
10 GCTCGCTTCA GTGGCAGTGG ATCTGGGACC TCTTACTCTC TCACAATCAG CCGAATGGAG 300  
GCTGAAGATG CTGCCACTTA TTACTGCCAG CAAAGGAGTA CTTACCCGCT CACGTTCCGT 360  
15 GCTGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420  
CCATCTGATG AGCAGTTGAA ATCTGGAACCT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480  
TATCCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540  
20 CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCCTG 600  
ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660  
25 GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 235 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1                5                      10                          15

5

Val Ile Met Ser Arg Gly Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile  
20 25 30

10

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser  
35 40 45

Ser Ser Val Thr Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser  
50 55 60

15

Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro  
65                      70                      75                      80

20

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95

Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg  
100 105 110

25

Ser Thr Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys  
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
130 135 140

30

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
145                      150                      155                      160

35

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
180 185 190

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Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
195 200 205

5 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

## 10 (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 765 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

25 ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60  
GTGCAGCTGC AGCARTCAGG GGCAGAGCTT GTGAGGTCAG GGGCCTCAGT CAAGTTGTCC 120  
TGCACAGCTT CTGGCTTCAA CATTAAAGAC AACTATATGC ACTGGGTGAA GCAGAGGCCT 180  
30 GAACAGGGCC TGGAGTGGAT TGCATGGATT GATCCTGAGA ATGGTGATAC TGAATATGCC 240  
CCGAAGTTCC GGGGCAAGGC CACTTTGACT GCAGACTCAT CCTCCAACAC AGCCTACCTG 300  
35 CACCTCAGCA GCCTGACATC TGAGGACACT GCCGTCTATT ACTGTCATGT CCTGATCTAT 360  
GCTGGTTATT TGGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCGCCGT GAGCTCGGCT 420

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AGCACCAAGG GACCATCGGT CTTCCCCCTG GCCCCCTGCT CCAGGAGCAC CTCCGAGAGC 480

ACAGCCGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

5 AACTCAGGCG CTCTGACCAG CGGCGTGCAC ACCTTCCCCG CTGTCCTACA GTCCTCAGGA 600

CTCTACTCCC TCAGCAGCGT CGTGACGGTG CCCTCCAGCA ACTTCGGCAC CCAGACCTAC 660

ACCTGCAACG TAGATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGACAGT TGAGCGCAA 720

10 TGTTGTGTCG AGTGCCACC GTGCCCGGCG CCACCTGTGG CCGGC 765

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly  
1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg  
20 25 30

Ser Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile  
35 40 45

Lys Asp Asn Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu  
50 55 60

Glu Trp Ile Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala  
65                      70                      75                      80

5      Pro Lys Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Ser Ser Ser Asn  
                        85                        90                        95

Thr Ala Tyr Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val  
100 105 110

10 Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr  
115 120 125

15 Trp Gly Gln Gly Thr Ser Val Ala Val Ser Ser Ala Ser Thr Lys Gly  
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser  
145 150 155 160

20 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
195 200 205

30 Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val  
210 215 220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys  
225 230 235 240

35 Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly  
245 250 255

[illegible]

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## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 121 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80

Tyr Ile Cys Asn Val Asn His Asn Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro  
 115 120



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## (2) INFORMATION FOR SEQ ID NO: 21:

5

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 369 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15

## (ii) MOLECULE TYPE: other nucleic acid

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCTT CCTCCAAGAG CACCTCTGGG 60  
GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 120  
25 TGGAAGTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180  
GGACTCTACT CCCTCAGCAG CGTGGTGACT GTGCCCTCCA GCAGCTTGGG CACCCAGACC 240  
TACATCTGCA ACGTGAATCA CAACCCAGC AACACCAAGG TCGACAAGAA AGTTGAGCCC 300  
30 AAATCTTG TG ACAAGACGCA CACGTGCCCC CCGTGCCCCG CTCCGGAAGT GCTGGGTGGC 360  
CCGTAATAG 369

## 35 (2) INFORMATION FOR SEQ ID NO: 22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids

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(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr  
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys  
85 90 95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
100 105 110

Pro Val Ala Gly  
115

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## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 348 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

15

GCTAGCACCA AGGGACCATC GGTCTTCCCC CTGGCCCCCT GCTCCAGGAG CACCTCCGAG 60

AGCACAGCCG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 120

20 TGGAACTCAG GCGCTCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180

GGACTCTACT CCCTCAGCAG CGTCGTGACG GTGCCCTCCA GCAACTTCGG CACCCAGACC 240

TACACCTGCA ACGTAGATCA CAAGCCCAGC AACACCAAGG TGGACAAGAC AGTTGAGCGC 300

25

AAATGTTGTG TCGAGTGCCC ACCGTGCCCC GCGCCACCTG TGGCCGGC 348

## (2) INFORMATION FOR SEQ ID NO: 24:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

## (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg  
 1 5 10 15

5 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30

10 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60

15 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95

20 Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro  
 100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg  
 115 120 125

25 Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys  
 130 135 140

30 Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro  
 145 150 155 160

Ala Pro Glu Leu Leu Gly Gly  
 165

35

(2) INFORMATION FOR SEQ ID NO: 25:

(1) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 501 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GCTAGCACCA AGGGCCCCATC GGTCTTCCCC CTGGCGCCCT GCTCCAGGAG CACCTCTGGG 60  
15 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 120  
TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 180  
GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 240  
20 TACACCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAG AGTGGAGCTG 300  
AAAACCCAC TTGGTGACAC AACTCACAG TGCCCTAGGT GTCCTGAACC TAAATCTTGT 360  
25 GACACACCTC CCCCCTGCCC ACGGTGCCCA GAGCCCAAAT CTTGCGACAC GCCCCACCG 420  
TGTCCTGAT GTCCTGAACC AAAGAGCTGT GACTACTCCAC CGCCCTGCCC GAGGTGCCCC 480  
GCACCTGAAC TCCTGGGAGG A 501

30

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

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(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Ser Ala Ser Ser Ser Val Thr Tyr Met His  
1 5 10

10 (2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ser Thr Ser Asn Leu Ala Ser  
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

5 Gln Gln Arg Ser Thr Tyr Pro Leu Thr  
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

10

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Asp Asn Tyr Met His  
1 5

30 (2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Phe Asn Ile Lys Asp Asn Tyr Met His

1

5

10 (2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe Arg

1

5

10

15

Gly

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear



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(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr  
1 5 10

10

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

25

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 34:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TCGAGAGATC TAAGCTTCCG CGGGAATTCC TCGAGGAGCT CCCCAGGGGA TCCGTCGACT 60

5

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

20

CTAGAGTCGA CGGATCCCCC GGGGAGCTCC TCGAGGAATT CCCGCGGAAG CTTAGATCTC 60

(2) INFORMATION FOR SEQ ID NO: 36:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

AAGCTTCCCG GGTATTAAAG CAGAACTTG

29

5 (2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

20 ACTAGTGGAT CCCAGACATG ATAAGATAC

29

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GGTCTATATA AGCAGAGCTG TCTGGCTAAC TAGAGAACC

39

00010050 00000000

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(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GGTTCTCTAG TTAGCCAGAC AGCTCTGCTT ATATAGACC

39

15 (2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

30 GGACTTTCCT ACTTGGCAG

19

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GGCAACTAGA AGGCACAGTC

20

10

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

25

AGCTTGCCGC CACCATGGAT TTTCAAGTGC AGATTTTCAG CTCCTGCTA ATCAGTGCTT

60

CAGTCATAAT GTCCCGC

77

30 (2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

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5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GGGACATTAT GACTGAAGCA CTGATTAGCA GGAAGCTGAA AATCTGCACT TGAAAATCCA 60

TGGTGGCGGC A 71

10

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

25

AGCTTGCCGC CACCATGAAG TTGTGGCTGA ACTGGATTTT CCTTGTAACA CTTTAAATG 60

G 61

30 (2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

PCT/GB97/01165

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5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

AATTCATTT AAAAGTGTTA CAAGGAAAAT CCAATTCAGC CACAACTTCA TGGTGGCGGC 60

A 61

10

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

AAGCTTCTCG AGATCAAACG GACTGTGGCT GCACCATCTG TCTTCATCTT CCCGCCATCT 60

GATGAGCAGT TGAAATCTGG AACTGCCTCT GTTGTGTGCC TGCTGAATAA CTTCTATCCC 120

30 AGAGAGGCCA AAGTACAGTG GAAGGTGGAT AACGCCCTCC AATCGGGTAA CTCCCAGGAG 180

AGTGTACAG AGCAGGACAG CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG 240

AGCAAAGCAG ACTACGAGAA ACACAAAGTC TACGCTGCG AAGTCACCCA TCAGGGCCTG 300

35

AGTTCGCCCC TCACAAAGAG CTTCAACAGG GGAGAGTGTT AATAGCCCGG GACTAGT 357

(2) INFORMATION FOR SEQ ID NO: 47:

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## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 381 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

15 GGAAGCTTGA GCTCGGCTAG CACCAAGGGA CCATCGGTCT TCCCCCTGGC CCCCTGCTCC 60  
AGGAGCACCT CCGAGAGCAC AGCCGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA 120  
CCGGTGACGG TGTCGTGGAA CTCAGGCGCT CTGACCAGCG GCGTGACAC CTTCCCGGCT 180  
20 GTCCTACAGT CCTCAGGACT CTA CTCCCTC AGCAGCGTCG TGACGGTGCC CTCCAGCAAC 240  
TTCGGCACCC AGACCTACAC CTGCAACGTA GATCACAAGC CCAGCAACAC CAAGGTGGAC 300  
25 AAGACAGTTG AGCGCAAATG TTGTGTCGAG TGCCCACCGT GCCCGGCGCC ACCTGTGGCC 360  
GGCTAATAGC CCGGGACTAG T 381

## (2) INFORMATION FOR SEQ ID NO: 48:

30

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 342 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

5 AAGCTTTCCC GCGGCGACAT CCAGATGACC CAGAGCCCAA GCAGCCTGAG CGCTAGCGTG 60  
GGTGACAGAG TGACCATCAC GTGTAGTGCC AGCTCAAGTG TAACTTACAT GCACTGGTAC 120  
CAGCAGAAGC CAGGTAAGGC TCCAAAGCTG CTGATCTACA GCACATCCAA CCTGGCTTCT 180  
10 GGTGTGCCAA GCAGATTCTC CGGAAGCGGT AGCGGCACCG ACTACACCTT CACCATCAGC 240  
AGCCTCCAGC CAGAGGATAT CGCCACCTAC TACTGCCAGC AGAGGAGTAC TTACCCGCTC 300  
ACGTTTCGGCC AAGGGACCAA GTCGAGATC AAACGGACTA GT 342  
15

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

30

GACATCCAGA TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60  
ATCACGTGTA GTGCCAGCTC AAGTGTA ACT TACATGCACT GGTACCAGCA GAAGCCAGGT 120  
35 AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180  
TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240

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GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300

ACCAAGCTCG AGATCAAACG G 321

5 (2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

20 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met  
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr  
35 40 45

30 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu  
65 70 75 80

35 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr  
85 90 95

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Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

100

105

(2) INFORMATION FOR SEQ ID NO: 51:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

15

ATGGATTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

CGCGGCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120

20 GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACCTACA TGCACTGGTA CCAGCAGAAG 180

CCAGGTAAGG CTCCAAAGCT GCTGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240

AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300

25

CCAGAGGATA TCGCCACCTA CTA CTGCCAG CAGAGGAGTA CTTACCCGCT CACGTTCGGC 360

CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

30 CCATCTGATG AGCAGTTGAA ATCTGGAAGT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTG 600

35

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

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## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 235 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## 10 (ii) MOLECULE TYPE: protein

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15

Val Ile Met Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser  
35 40 45

Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
50 55 60

Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile  
85 90 95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg  
100 105 110

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Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
115 120 125

5            Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
             130                            135                            140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
145                      150                      155                      160

10 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

25 (2) INFORMATION FOR SEQ. ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GAAGCTTGGA ATTCAGTGTG AGGTGCAGCT GCAGCAGAGC GGTCCAGGTC TCGTACGGCC 60  
5 TAGCCAGACC CTGAGCCTCA CGTGCACCGC ATCTGGCTTC AACATTAAGG ACAATTACAT 120  
GCACTGGGTG AGACAGCCAC CTGGACGAGG CCTTGAGTGG ATTGGATGGA TTGACCCTGA 180  
GAATGGTGAC ACTGAGTACG CACCTAAGTT TCGCGGCCGC GTGACAATGC TGGCAGACAC 240  
10 TAGTAAGAAC CAGTTCAGCC TGAGACTCAG CAGCGTGACA GCCGCCGACA CCGCGGTCTA 300  
TTATTGTCAC GTCCTGATAT ACGCCGGGTA TCTGGCAATG GACTACTGGG GCCAAGGGAC 360  
15 CCTCGTCACC GTGAGCTCGA CTAGT 385

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

30 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60  
ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120  
CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180  
35 GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACA CTAGTAAGAA CCAGTTCAGC 240  
CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

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TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

5 (2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

20 Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
20 25 30

25 Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
35 40 45

30 Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
50 55 60

Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser  
65 70 75 80

35 Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln  
100 105 110

5 Gly Thr Leu Val Thr Val Ser Ser  
115 120

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- 10
- (A) LENGTH: 765 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- 15
- (ii) MOLECULE TYPE: other nucleic acid

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ATGAAGTTGT	GGCTGAACTG	GATTTTCCTT	GTAACACTTT	TAAATGGAAT	TCAGTGTGAG	60
GTGCAGCTGC	AGCAGAGCGG	TCCAGGTCTC	GTACGGCCTA	GCCAGACCCT	GAGCCTCAGC	120
TGCACCGCAT	CTGGCTTCAA	CATTAAGGAC	AATTACATGC	ACTGGGTGAG	ACAGCCACCT	180
GGACGAGGCC	TTGAGTGGAT	TGGATGGATT	GACCCTGAGA	ATGGTGACAC	TGAGTACGCA	240
CCTAAGTTTC	GCGGCCGCGT	GACAATGCTG	GCAGACACTA	GTAAGAACCA	G TTCAGCCTG	300
AGACTCAGCA	GCGTGACAGC	CGCCGACACC	GCGGTCTATT	ATTGTACAGT	CCTGATATAC	360
GCCGGGTATC	TGGCAATGGA	CTACTGGGGC	CAAGGGACCC	TCGTCACCGT	GAGCTCGGCT	420
AGCACCAAGG	GACCATCGGT	CTTCCCCCTG	GCCCCCTGCT	CCAGGAGCAC	CTCCGAGAGC	480
ACAGCCGCCC	TGGGCTGCCT	GGTCAAGGAC	TACTTCCCCG	AACCGGTGAC	GGTGTCGTGG	540



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AACTCAGGCG CTCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600  
 CTCTACTCCC TCAGCAGCGT CGTGACGGTG CCCTCCAGCA ACTTCGGCAC CCAGACCTAC 660  
 5 ACCTGCAACG TAGATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGACAGT TGAGCGCAAA 720  
 TGTGTGTGTCG AGTGCCCAACC GTGCCCGGCG CCACCTGTGG CCGGC 765

10 (2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids  
 (B) TYPE: amino acid  
 15 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

25 Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly  
 1 5 10 15  
 Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg  
 20 25 30  
 30 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile  
 35 40 45  
 Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu  
 35 50 55 60  
 Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala  
 65 70 75 80

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Pro Lys Phe Arg Gly Arg Val Thr M t Leu Ala Asp Thr Ser Lys Asn  
 85 90 95

5 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr  
 115 120 125

10 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 130 135 140

15 Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser  
 145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
 165 170 175

20 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
 180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 195 200 205

25 Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val  
 210 215 220

30 Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys  
 225 230 235 240

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly  
 245 250 255

35 (2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGCGACATCC AGCTGACCCA GAGCCCAAGC AGCCTGAGCG

40

10

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

25

CTAGCGCTCA GGCTGCTTGG GCTCTGGGTC AGCTGGATGT CGCCGC

46

(2) INFORMATION FOR SEQ ID NO: 60:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GACATCCAGC TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60  
 5 ATCACGTGTA GTGCCAGCTC AAGTGTA ACT TACATGCACT GGTACCAGCA GAAGCCAGGT 120  
 AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180  
 TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240  
 10 GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCAGTT CGGCCAAGGG 300  
 ACCAAGCTCG AGATCAAACG G 321

15 (2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

30 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met  
 20 25 30  
 35 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr  
 35 40 45

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Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser

50

55

60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu

5

65

70

75

80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr

85

90

95

10

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

100

105

(2) INFORMATION FOR SEQ ID NO: 62:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GGCCAGATCG TGCTGACCCA GAGCCCAAGC AGCCTGAGCG

40

30 (2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CTAGCGCTCA GGCTGCTTGG GCTCTGGGTC AGCACGATCT GGCCGC

46

(2) INFORMATION FOR SEQ ID NO: 64:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

25

CAGATCGTGC TGACCCAGAG CCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60

ATCACGTGTA GTGCCAGCTC AAGTGTA ACT TACATGCACT GGTACCAGCA GAAGCCAGGT 120

AAGGCTCCAA AGCTGCTGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180

30 TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240

GATATCGCCA CCTACTACTG. CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300

ACCAAGCTCG AGATCAAACG G 321

35

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- 135 -

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met

20

25

30

20

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr

35

40

45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser

50

55

60

25

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu

65

70

75

80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr

30

85

90

95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

100

105

35 (2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

- 136 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CGTATTAGTC ATCGCTATTA CC

22

(2) INFORMATION FOR SEQ ID NO: 67:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

20

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GTTGGATGTG CTGTAGATCC ACAGCTTTGG AGCCTTACC

39

(2) INFORMATION FOR SEQ ID NO: 68:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid



- 137 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

5

TCCGTTTGAT CTCGAGCTTG G

21

(2) INFORMATION FOR SEQ ID NO: 69:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GGTAAGGCTC CAAAGCTGTG GATCTACAGC ACATCCAAC

39

25 (2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35

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- 138 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GACATCCAGA TGACCCAGAG CCCAAGCAGC CTGAGCGCTA GCGTGGGTGA CAGAGTGACC 60  
 5 ATCACGTGTA GTGCCAGCTC AAGTGTA ACT TACATGCACT GGTACCAGCA GAAGCCAGGT 120  
 AAGGCTCCAA AGCTGTGGAT CTACAGCACA TCCAACCTGG CTTCTGGTGT GCCAAGCAGA 180  
 TTCTCCGGAA GCGGTAGCGG CACCGACTAC ACCTTCACCA TCAGCAGCCT CCAGCCAGAG 240  
 10 GATATCGCCA CCTACTACTG CCAGCAGAGG AGTACTTACC CGCTCACGTT CGGCCAAGGG 300  
 ACCAAGCTCG AGATCAAACG G 321

15 (2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids  
 (B) TYPE: amino acid  
 20 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

30 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met  
 20 25 30

35

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr  
 35 40 45

- 139 -

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
 50 55 60

Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu  
 5 65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Leu Thr  
 85 90 95

10 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
 100 105

## (2) INFORMATION FOR SEQ ID NO: 72:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CCTTGAGTGG ATTGCATGGA TTGACCCTGA GAATGGTGAC ACTGAGTACG CACCTAAGTT 60

30 TCGC 64

## (2) INFORMATION FOR SEQ ID NO: 73:

- 35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid

- 140 -

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

10

GGCCGCGAAA CTTAGGTGCG TACTCAGTGT CACCATTCTC AGGGTCAATC CATGCAATCC 60

ACTCAAGG 68

15 (2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

30 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

35

GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACA CTAGTAAGAA CCAGTTCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCTTCGTAC CGTGAGCTCG 360

(2) INFORMATION FOR SEQ ID NO: 75:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

## (ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

20

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
1                5                      10                          15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
20 25 30

25

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
35 40 45

Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
50 55 60

30

Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser  
65 70 75 80

35

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln  
100 105 110

- 142 -

Gly Thr Leu Val Thr Val Ser Ser

115

120

## 5 (2) INFORMATION FOR SEQ ID NO: 76:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

20 GGCCGCGTGA CAATGCTGGC AGACTCAAGT AAGAACCAGG CCAGCCTGAG ACTCAGCAGC 60

GTGACAGCCG CCGACACCGC 80

## (2) INFORMATION FOR SEQ ID NO: 77:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

35

- 143 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GGTGTCCGCG GCTGTCACGC TGCTGAGTCT CAGGCTGGCC TGGTCTTAC TTGAGTCTGC 60

5 CAGCATTGTC ACGC 74

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

25 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60

ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

30

GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

35 TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

T022201 6507660

- 144 -

## (2) INFORMATION FOR SEQ ID NO: 79:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
20 25 30

Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
50 55 60

Arg Gly Arg Val Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser  
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120



- 145 -

## (2) INFORMATION FOR SEQ ID NO: 80:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## 10 (ii) MOLECULE TYPE: other nucleic acid

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60  
ACGTGCACCG CATCTGGCTT CAACATTAA GACAATTACA TGCACTGGGT GAGACAGCCA 120  
20 CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180  
GCACCTAAGT TTCGCGGCCG CGTGACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240  
25 CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300  
TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

## 30 (2) INFORMATION FOR SEQ ID NO: 81:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

5      Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
       1                                5                                10                                15

      Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
                               20                                25                                30

10      Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
                               35                                40                                45

      Ala Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
                               50                                55                                60

15      Arg Gly Arg Val Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser  
                               65                                70                                75                                80

      Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
                               85                                90                                95

20      His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln  
                               100                                105                                110

25      Gly Thr Leu Val Thr Val Ser Ser  
                               115                                120

(2) INFORMATION FOR SEQ ID NO: 82:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

5

GGCCGCGCCA CAATGCTGGC AGACACTAGT AAGAACCAGT TCAGCCTGAG ACTCAGCAGC 60

GTGACAGCCG CCGACACCGC 80

10 (2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

25 GGTGTCGGCG GCTGTCACGC TGCTGAGTCT CAGGCTGAAC TGGTTCTTAC TAGTGTCTGC 60

CAGCATTGTG GCGC 74

(2) INFORMATION FOR SEQ ID NO: 84:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

FOUO 05004000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

	GAGGTGCAGC	TGCAGCAGAG	CGGTCCAGGT	CTCGTACGGC	CTAGCCAGAC	CCTGAGCCTC	60
5							
	ACGTGCACCG	CATCTGGCTT	CAACATTAAG	GACAATTACA	TGCACTGGGT	GAGACAGCCA	120
	CCTGGACGAG	GCCTTGAGTG	GATTGGATGG	ATTGACCCTG	AGAATGGTGA	CACTGAGTAC	180
10	GCACCTAAGT	TTCGCGGCCG	CGCCACAATG	CTGGCAGACA	CTAGTAAGAA	CCAGTTCAGC	240
	CTGAGACTCA	GCAGCGTGAC	AGCCGCCGAC	ACCGCGGTCT	ATTATTGTCA	CGTCCTGATA	300
	TACGCCGGGT	ATCTGGCAAT	GGACTACTGG	GGCCAAGGGA	CCCTCGTCAC	CGTGAGCTCG	360

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
1                5                      10                          15

35 Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
20 25 30

[illegible]

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Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
 35 40 45

5 Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
 50 55 60

Arg Gly Arg Ala Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser  
 65 70 75 80

10 Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

15 His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
 115 120

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GGCCGCGCCA CAATGCTGGC AGACTCAAGT AAGAACCAGG CCAGCCTGAG ACTCAGCAGC 60

GTGACAGCCG CCGACACCGC 80

- 150 -

## (2) INFORMATION FOR SEQ ID NO: 87:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GGTGTGCGCG GCTGTCACGC TGCTGAGTCT CAGGCTGGCC TGGTCTTAC TTGAGTCTGC 60  
CAGCATTGTG GCGC 74

## 20 (2) INFORMATION FOR SEQ ID NO: 88:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

35 GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60  
ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120

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CCTGGACGAG GCCTTGAGTG GATTGGATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180

GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240

5 CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGGTCT ATTATTGTCA CGTCCTGATA 300

TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360

## 10 (2) INFORMATION FOR SEQ ID NO: 89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

25 Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn  
20 25 30

30 Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe  
35 50 55 60

Arg Gly Arg Ala Thr Met Leu Ala Asp Ser Ser Lys Asn Gln Ala Ser  
65 70 75 80

- 152 -

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

5 His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

10

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GAGGTGCAGC TGCAGCAGAG CGGTCCAGGT CTCGTACGGC CTAGCCAGAC CCTGAGCCTC 60  
ACGTGCACCG CATCTGGCTT CAACATTAAG GACAATTACA TGCACTGGGT GAGACAGCCA 120  
CCTGGACGAG GCCTTGAGTG GATTGCATGG ATTGACCCTG AGAATGGTGA CACTGAGTAC 180  
GCACCTAAGT TTCGCGGCCG CGCCACAATG CTGGCAGACT CAAGTAAGAA CCAGGCCAGC 240  
CTGAGACTCA GCAGCGTGAC AGCCGCCGAC ACCGCGSTCT ATTATTGTCA CGTCCTGATA 300  
TACGCCGGGT ATCTGGCAAT GGACTACTGG GGCCAAGGGA CCCTCGTCAC CGTGAGCTCG 360



(i) SEQUENCE CHARACTERISTICS:

5

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

15

3

5

10

15

20

20

25

30

35

40

45

25

50

55

60

65

70

75

80

30

85

90

95

35

100

105

110

115

120

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(2) INFORMATION FOR SEQ ID NO: 92:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 780 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

15 ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60  
GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCCT GAGCCTCACG 120  
20 TGCACCGCAT CTGGCTTCAA CATTAAAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180  
GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240  
CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300  
25 AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360  
GCCGGGTATC TGGCAATGGA CTACTGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCC 420  
30 TCCACCAAGG GCCCATCGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC CTCTGGGGGC 480  
ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540  
AACTCAGGCG CCCTGACCAG CGGCGTGAC ACCTTCCCCG CTGTCCTACA GTCCTCAGGA 600  
35 CTCTACTCCC TCAGCAGCGT GGTGACTGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC 660  
ATCTGCAACG TGAATCACAA CCCAGCAAC ACCAAGGTCG ACAAGAAAGT TGAGCCCCAA 720

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TCTTGTGACA AGACGCACAC GTGCCC GCCG TGCCCGGCTC CGGAAC TGCT GGGTGGCCCCG

780

## 5 (2) INFORMATION FOR SEQ ID NO: 93:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

20

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly  
 1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg  
 20 25 30

25

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile  
 35 40 45

30

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu  
 50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala  
 65 70 75 80

35

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn  
 85 90 95

- 156 -

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr  
 5 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly  
 10 145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
 15 165 170 175

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
 180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 20 195 200 205

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val  
 210 215 220

Asn His Asn Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys  
 25 225 230 235 240

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu  
 245 250 255

30 Leu Gly Gly Pro  
 260

(2) INFORMATION FOR SEQ ID NO: 94:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

10

ATGAAGTTGT GGCTGAACTG GATTTTCCTT GTAACACTTT TAAATGGAAT TCAGTGTGAG 60

GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC GTACGGCCTA GCCAGACCTT GAGCCTCACG 120

15 TGCACCGCAT CTGGCTTCAA CATTAAAGGAC AATTACATGC ACTGGGTGAG ACAGCCACCT 180

GGACGAGGCC TTGAGTGGAT TGGATGGATT GACCCTGAGA ATGGTGACAC TGAGTACGCA 240

CCTAAGTTTC GCGGCCGCGT GACAATGCTG GCAGACACTA GTAAGAACCA GTTCAGCCTG 300

20

AGACTCAGCA GCGTGACAGC CGCCGACACC GCGGTCTATT ATTGTCACGT CCTGATATAC 360

GCCGGGTATC TGGCAATGGA CTACTGGGGC CAAGGGACCC TCGTCACCGT GAGCTCGGCT 420

25 AGCACCAAGG GCCCATCGGT CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC CTCTGGGGGC 480

ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 540

AACTCAGGCG CCCTGACCAG CGGCGTGAC ACCTTCCCGG CTGTCCTACA GTCCTCAGGA 600

30

CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC 660

ACCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAGAGT GGAGCTGAAA 720

35 ACCCCACTCG GTGACACAAC TCACACGTGC CCTAGGTGTC CTGAACCTAA ATCTTGTGAC 780

ACACCTCCCC CGTGCCACG GTGCCAGAG CCCAAATCTT GCGACACGCC CCCACCGTGT 840

[illegible]

- 158 -

CCCAGATGTC CTGAACCAA GAGCTGTGAC ACTCCACCGC CCTGCCCGAG GTGCCCAGCA 900

CCTGAACTCC TGGGAGGG 918

5 (2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

20 Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly  
1 5 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg  
20 25 30

25

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile

35 40 45

30 Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu  
50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala  
65                      70                      75                      80

35

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr S r Lys Asn

85 90 95

[illegible]

- 160 -

Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu  
290 295 300

Gly Gly

5 305

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 705 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

CGCGGCCAGA TCGTGCTGAC CCAGAGCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120

25  
GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACCTTACA TGCACTGGTA CCAGCAGAAG 180

CCAGGTAAGG CTCCAAAGCT GCTGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240

30 AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300

CCAGAGGATA TCGCCACCTA CTACTGCCAG CAGAGGAGTA CTTACCCGCT CACGTTTCGGC 360

CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCCG 420

35  
CCATCTGATG AGCAGTTGAA ATCTGGAAC TGCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCCAGAG AGGCCAAAGT ACAGTGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

[illegible]



CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCCTG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 97:

## 10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1                5                      10                          15

25  
Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ser Ser  
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser  
30                35                      40                                  45

Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala  
50 55 60

35 Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80

- 162 -

Ser Arg Phe Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile  
 85 90 95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg  
 5 100 105 110

Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
 115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
 10 130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
 145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
 165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
 20 180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
 195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- 163 -

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATGGATTTTC AAGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCTTCAGT CATAATGTCC 60

10 CGCGGCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCTAGCGT GGGTGACAGA 120

GTGACCATCA CGTGTAGTGC CAGCTCAAGT GTAACCTTACA TGCACTGGTA CCAGCAGAAG 180

CCAGGTAAGG CTCCAAAGCT GTGGATCTAC AGCACATCCA ACCTGGCTTC TGGTGTGCCA 240

15 AGCAGATTCT CCGGAAGCGG TAGCGGCACC GACTACACCT TCACCATCAG CAGCCTCCAG 300

CCAGAGGATA TCGCCACCTA CTA CTGCCAG CAGAGGAGTA CTTACCCGCT CACGTTCCGC 360

20 CAAGGGACCA AGCTCGAGAT CAAACGGACT GTGGCTGCAC CATCTGTCTT CATCTTCCCG 420

CCATCTGATG AGCAGTTGAA ATCTGGA ACT GCCTCTGTTG TGTGCCTGCT GAATAACTTC 480

TATCCAGAG AGGCCAAAGT ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC 540

25 CAGGAGAGTG TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTCG 600

ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT CACCCATCAG 660

30 GGCCTGAGTT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG AGTGT 705

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

10

15

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35

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
145                      150                      155                      160

- 165 -

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
 165 170 175

5 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
 180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
 195 200 205

10 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
 210 215 220

15 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: other nucleic acid

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CCCAGCACCT GAACTCCTGG GAGGAGCAAC AGGACACAGT TATGAGAAGT ACAA

54

(2) INFORMATION FOR SEQ ID NO: 101:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

PCT/GB97/01165

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

10 GGGGGTCTAG ATTATTAGTA CAGGTGTTCC AGGACGTAGC TGGCAACATA

50

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

25

GGGGGAGCTC GGCTAGCACC AAGGGCCCAT CGGTCTTCCC CCTGGC

46

(2) INFORMATION FOR SEQ ID NO: 103:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTGTACTTCT CATAACTGTG TCCTGTTGCT CCTCCCAGGA GTTCAGGTGC TGGGC

55

5 (2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

20 GCCTGTGCTC AATATTGATG G

21

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

- 168 -

GGAGAAAGCC ATATCTGCCT G

21

(2) INFORMATION FOR SEQ ID NO: 106:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TCGCTATTAC CATGGTGATG CGGTTTGGC

30

20 (2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GGCTGGATTC TCAGTGGCGA CTT

23

35

(2) INFORMATION FOR SEQ ID NO: 108:



- 169 -

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

CACAACAGAG GCAGTTCC

## (2) INFORMATION FOR SEQ ID NO: 109:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CACCTTCACC ATCAGCAGCC

## (2) INFORMATION FOR SEQ ID NO: 110:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

10 GGACCTGCTG CAGAGTCTG

19

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GGCTGCAGGA ATTCTTATTA TAGACGAACC CGGCTATCAA ACTGAGC

47

(2) INFORMATION FOR SEQ ID NO: 112:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1870 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

1 AAGCTTGCCG CCACCATGAA GTTGTGGCTG AACTGGATTT TCCTTGTAAC ACTTTTAAAT 60

5 GGAATTCAGT GTGAGGTGCA GCTGCAGCAG AGCGGTCCAG GTCTCGTACG GCCTAGCCAG 120

ACCCTGAGCC TCACGTGCAC CGCATCTGGC TTCAACATTA AGGACAATTA CATGCACTGG 180

GTGAGACAGC CACCTGGACG AGGCCTGAG TGGATTGGAT GGATTGACCC TGAGAATGGT 240

10 GACACTGAGT ACGCACCTAA GTTTCGCGGC CGCGTGACAA TGCTGGCAGA CACTAGTAAG 300

AACCAGTTCA GCCTGAGACT CAGCAGCGTG ACAGCCGCCG ACACCGCGGT CTATTATTGT 360

15 CACGTCCTGA TATACGCCGG GTATCTGGCA ATGGACTACT GGGGCCAAGG GACCCTCGTC 420

ACCGTGAGCT CGGCTAGCAC CAAGGGCCCA TCGGTCTTCC CCCTGGCGCC CTGCTCCAGG 480

AGCACCTCTG GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG 540

20 GTGACGGTGT CGTGGAATC AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC 600

CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG 660

25 GGCACCCAGA CCTACACCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGGACAAG 720

AGAGTGAGC TGAAAACCCC ACTCGGTGAC ACAACTCACA CGTGCCCTAG GTGTCCTGAA 780

CCTAAATCTT GTGACACACC TCCCCCGTGC CCACGGTGCC CAGAGCCCAA ATCTTGCGAC 840

30 ACGCCCCCAC CGTGTCCTAG ATGTCCTGAA CCAAAGAGCT GTGACACTCC ACCGCCCTGC 900

CCGAGGTGCC CAGCACCTGA ACTCCTGGA GGAGCAACAG GACACAGTTA TGAGAAGTAC 960

35 AACAAAGTGGG AAACGATAGA GGCTTGGACT CAACAAGTCG CCACTGAGAA TCCAGCCCTC 1020

ATCTCTCGCA GTGTTATCGG AACCACATTT GAGGGACGCG CTATTTACCT CCTGAAGGTT 1080

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GGCAAAGCTG GACAAAATAA GCCTGCCATT TTCATGGACT GTGGTTTCCA TGCCAGAGAG 1140  
TGGATTTCTC CTGCATTCTG CCAGTGGTTT GTAAGAGAGG CTGTTCTGAC CTATGGACGT 1200  
5 GAGATCCAAG TGACAGAGCT TCTCGACAAG TTAGACTTTT ATGTCCTGCC TGTGCTCAAT 1260  
ATTGATGGCT ACATCTACAC CTGGACCAAG AGCCGATTTT GGAGAAAGAC TCGCTCCACC 1320  
CATACTGGAT CTAGCTGCAT TGGCACAGAC CCCAACAGAA ATTTTGATGC TGGTTGGTGT 1380  
10 GAAATTGGAG CCTCTCGAAA CCCCTGTGAT GAAACTTACT GTGGACCTGC CGCAGAGTCT 1440  
GAAAAGGAGA CCAAGGCCCT GGCTGATTTC ATCCGCAACA AACTCTCTTC CATCAAGGCA 1500  
15 TATCTGACAA TCCACTCGTA CTCCCAAATG ATGATCTACC CTTACTCATA TGCTTACAAA 1560  
CTCGGTGAGA ACAATGCTGA GTTGAATGCC CTGGCTAAAG CTA CTGTGAA AGAACTTGCC 1620  
TCACTGCACG GCACCAAGTA CACATATGGC CCGGGAGCTA CAACAATCTA TCCTTCTGCT 1680  
20 GGGACTTCTA AAGACTGGSC TTATGACCAA GGAATCAGAT ATTCCTTCAC CTTTGAACCT 1740  
CGAGATACAG GCAGATATGG CTTTCTCCTT CCAGAATCCC AGATCCGGGC TACCTGCGAG 1800  
25 GAGACCTTCC TGGCAATCAA GTATGTTGCC AGCTACGTCC TGAACACCT GTACTAATAA 1860  
TCTAGAGAGA 1870.

(2) INFORMATION FOR SEQ ID NO: 113:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly  
 1 5 10 15  
 Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg  
 20 25 30  
 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile  
 35 40 45  
 Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu  
 50 55 60  
 Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala  
 65 70 75 80  
 Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn  
 85 90 95  
 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 100 105 110  
 Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr  
 115 120 125  
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
 130 135 140  
 Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly  
 145 150 155 160  
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val  
 165 170 175  
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe  
 180 185 190

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Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
 195 200 205

5 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val  
 210 215 220

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys  
 225 230 235 240

10 Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro  
 245 250 255

15 Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys  
 260 265 270

Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser  
 275 280 285

20 Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu  
 290 295 300

Gly Gly Ala Thr Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr  
 305 310 315 320

25 Ile Glu Ala Trp Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile  
 325 330 335

30 Ser Arg Ser Val Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu  
 340 345 350

Leu Lys Val Gly Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp  
 355 360 365

35 Cys Gly Phe His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp  
 370 375 380

- 175 -

Phe Val Arg Glu Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr  
385                      390                      395                      400

5

Asp Gly Tyr Ile Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr  
420 425 430

10

15

Asp Glu Thr Tyr Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys  
465 470 475 480

20

Leu Thr Ile His Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr  
500 505 510

25

Ala Thr Val Lys Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr  
530 535 540

30

Gly Pro Gly Ala Thr Thr Ile Tyr Pro Ser Ala Gly Thr Ser Lys Asp  
545                      550                      555                      560

35

Trp Ala Tyr Asp Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg  
565 570 575

Asp Thr Gly Arg Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala  
580 585 590

- 176 -

Thr Cys Glu Glu Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val  
 595 600 605

5 Leu Glu His Leu Tyr  
 610

## (2) INFORMATION FOR SEQ ID NO: 114:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 96 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

His His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn  
 1 5 10 15

25 Val Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr  
 20 25 30

Thr Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro  
 35 40 45

30 His Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val  
 50 55 60

35 Glu Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser  
 65 70 75 80

Asn Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Leu  
 85 90 95

114: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96



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## (2) INFORMATION FOR SEQ ID NO: 115:

## 5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

## (ii) MOLECULE TYPE: other nucleic acid

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GAGCTCGGCT AGCACCAAGG GCCCATCGGT CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC 60

20 CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC 120

GGTGTCTGG AACTCAGGCG CCCTGACCAG CGGCGTGAC ACCTTCCCGG CTGTCCTACA 180

GTCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG CCCTCCAGCA GCTTGGGCAC 240

25 CCAGACCTAC ACCTGCAACG TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAGAGT 300

GGAGCTGAAA ACCCACTCG GTGACACAAC TCACACGTGC CCTAGGTGTC CTGAACCTAA 360

30 ATCTTGTGAC ACACCTCCCC CGTGCCCACG GTGCCCAGAG CCCAAATCTT GCGACACGCC 420

CCCACCGTGT CCCAGATGTC CTGAACCAA GAGCTGTGAC ACTCCACCGC CCTGCCCCGAG 480

GTGCCCAGCA CCTGAACTCC TGGGAGGGTA ATAGCCCCGGG 520

35

## (2) INFORMATION FOR SEQ ID NO: 116:

## (i) SEQUENCE CHARACTERISTICS:

- 178 -

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GTTATTACTC GCTGCCCAAC CAGCCATGGC G

31

15 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

30 GCAGCAGGAT AGATTGTTGT AGC

23

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

- 179 -

(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

CCGGAATTCT TATTAGTTCA GGTCTCTCTC AGAGATCAGC TTCTGCTCCT CGAACTCATG 60  
GTGGTGATGG TGGTGGTACA GGTGTTCC 88

(2) INFORMATION FOR SEQ ID NO: 119:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CAATCTATCC TGCTGCTGGG ACTTCTAAAG 30

30 (2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

-180-

(ii) MOLECULE TYPE: ther nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

GATTGTTGTA GCTCCCGGGC

20

10 (2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

GGAGCTACAA CAATCTATCC TTCTGCTGGG

30

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

- 181 -

ACGGCACCAA GTACACATAT GG

22

(2) INFORMATION FOR SEQ ID NO: 123:

## 5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ACGAGAATTC GACCGCTCTG CTGCAGCTGC ACCTCGGAAC CGCCACCGCT GCCACCGCCA 60

20 GAACCGCCAC CGTACAGGTG TTCCAGGACG 90

(2) INFORMATION FOR SEQ ID NO: 124:

## 25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2154 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

35 ATGTTGGCAC TCTTGGTTCT GGTGACTGTG GCCCTGGCAT CTGCTCATCA TGGTGGTGAG 60

CACTTTGAAG GCGAGAAGGT GTCCGTGTT AACGTTGAAG ATGAAAATCA CATTAAACATA 120

FOUO 20 0500 0500

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	ATCCGCGAGT TGGCCAGCAC GACCCAGATT GACTTCTGGA AGCCAGATTC TGTCACACAA	180
	ATCAAACCTC ACAGTACAGT TGA CTTCCTGT GTTAAAGCAG AAGATACTGT CACTGTGGAG	240
5	AATGTTCTAA AGCAGAATGA ACTACAATAC AAGGTACTGA TAAGCAACCT GAGAAATGTG	300
	GTGGAGGCTC AGTTTGATAG CCGGGTTCGT GCAACAGGAC ACAGTTATGA GAAGTACAAC	360
	AAGTGGGAAA CGATAGAGGC TTGGACTCAA CAAGTCGCCA CTGAGAATCC AGCCCTCATC	420
10	TCTCGCAGTG TTATCGGAAC CACATTTGAG GGACGCGCTA TTTACCTCCT GAAGGTTGGC	480
	AAAGCTGGAC AAAATAAGCC TGCCATTTTC ATGGACTGTG GTTTCCATGC CAGAGAGTGG	540
15	ATTTCTCCTG CATTCTGCCA GTGGTTTGTA AGAGAGGCTG TTCGTACCTA TGGACGTGAG	600
	ATCCAAGTGA CAGAGCTTCT CGACAAGTTA GACTTTTATG TCCTGCCTGT GCTCAATATT	660
	GATGGCTACA TCTACACCTG GACCAAGAGC CGATTTTGGA GAAAGACTCG CTCCACCCAT	720
20	ACTGGATCTA GCTGCATTGG CACAGACCCC AACAGAAATT TTGATGCTGG TTGGTGTGAA	780
	ATTGGAGCCT CTCGAAACCC CTGTGATGAA ACTTACTGTG GACCTGCCGC AGAGTCTGAA	840
25	AAGGAGACCA AGGCCCTGGC TGATTTTCATC CGCAACAAAC TCTCTTCCAT CAAGGCATAT	900
	CTGACAATCC ACTCGTACTC CCAAATGATG ATCTACCCTT ACTCATATGC TTACAAACTC	960
	GGTGAGAACA ATGCTGAGTT GAATGCCCTG GCTAAAGCTA CTGTGAAAGA ACTTGCCTCA	1020
30	CTGCACGGCA CCAAGTACAC ATATGGCCCC GGAGCTACAA CAATCTATCC TTCTGCTGGG	1080
	ACTTCTAAAG ACTGGGCTTA TGACCAAGGA ATCAGATATT CCTTCACCTT TGAACCTCGA	1140
35	GATACAGGCA GATATGGCTT TCTCCTTCCA GAATCCCAGA TCCGGGCTAC CTGCGAGGAG	1200
	ACCTTCCTGG CAATCAAGTA TGTGGCCAGC TACGTCCTGG AACACCTGTA CGGTGGCGGT	1260

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TCTGGCGGTG GCAGCGGTGG CGGTTCCGAG GTGCAGCTGC AGCAGAGCGG TCCAGGTCTC 1320  
GTACGGCCTA GCCAGACCCT GAGCCTCAGC TGCACCGCAT CTGGCTTCAA CATTAAAGGAC 1380  
AATTACATGC ACTGGGTGAG ACAGCCACCT GGACGAGGCC TTGAGTGGAT TGGATGGATT 1440  
GACCCTGAGA ATGGTGACAC TGAGTACGCA CCTAAGTTTC GCGGCCCGCT GACAATGCTG 1500  
GCAGACACTA GTAAGAACCA GTTCAGCCTG AGACTCAGCA GCGTGACAGC CGCCGACACC 1560  
GCGGTCTATT ATTGTCACGT CCTGATATAC GCCGGGTATC TGGCAATGGA CTACTGGGGC 1620  
CAAGGGACCC TCGTCACCGT GAGCTCGGCT AGCACCAAGG GCCCATCGGT CTTCCCCCTG 1680  
GCGCCCTGCT CCAGGAGCAC CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC 1740  
TACTTCCCCG AACCGGTGAC GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGAC 1800  
ACCTTCCCCG CTGTCCTACA GTCCTCAGGA CTCTACTCCC TCAGCAGCGT GGTGACCGTG 1860  
CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ACCTGCAACG TGAATCACAA GCCCAGCAAC 1920  
ACCAAGGTGG ACAAGAGAGT GGAGCTGAAA ACCCCACTCG GTGACACAAC TCACACGTGC 1980  
CCTAGGTGTC CTGAACCTAA ATCTTGTGAC ACACCTCCCC CGTGCCCACG GTGCCCAGAG 2040  
CCCAAATCTT GCGACACGCC CCCACCGTGT CCCAGATGTC CTGAACCAAA GAGCTGTGAC 2100  
ACTCCACCGC CCTGCCCAGG GTGCCCAGCA CCTGAACTCC TGGGAGGGTA ATAG 2154

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Met Leu Ala Leu Leu Val Leu Val Thr Val Ala Leu Ala Ser Ala His  
1                5                      10                          15

10

His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn Val  
20 25 30

15

Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr Thr  
35 40 45

Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro His  
50 55 60

20

Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val Glu  
65                      70                      75                      80

Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser Asn  
85 90 95

25

Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Ala Thr  
100 105 110

30

Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr Ile Glu Ala Trp  
115 120 125

Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile Ser Arg Ser Val  
130 135 140

35

Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu Leu Lys Val Gly  
145                      150                      155                      160

[illegible]



Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp Cys Gly Phe His  
165 170 175

Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp Phe Val Arg Glu  
180 185 190

Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr Glu Leu Leu Asp  
195 200 205

10      Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile Asp Gly Tyr Ile  
          210                          215                          220

Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr Arg Ser Thr His  
225                    230                    235                    240

Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg Asn Phe Asp Ala  
245 250 255

Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys Asp Glu Thr Tyr  
260 265 270

Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys Ala Leu Ala Asp  
275 280 285

25 Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr Leu Thr Ile His  
290 295 300

Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr Ala Tyr Lys Leu  
305 310 315 320

Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys Ala Thr Val Lys  
325 330 335

Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr Gly Pro Gly Ala  
35                      340                      345                      350

Thr Thr Ile Tyr Pro Ser Ala Gly Thr Ser Lys Asp Trp Ala Tyr Asp  
355 360 365

Gln Gly Ile Arg Tyr Ser Phe Thr	Glu Leu Arg Asp Thr Gly Arg	
370	375	380
Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala Thr Cys Glu Glu		
385	390	395 400
Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val Leu Glu His Leu		
405	410	415
Tyr Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Val Gln		
420	425	430
Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser		
435	440	445
Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Asn Tyr Met His		
450	455	460
Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly Trp Ile		
465	470	475 480
Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe Arg Gly Arg		
485	490	495
Val Thr Met Leu Ala Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu		
500	505	510
Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys His Val Leu		
515	520	525
Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu		
530	535	540
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu		
545	550	555 560

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Ala Pr Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
 565 570 575

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
 580 585 590

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
 595 600 605

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser  
 610 615 620

Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn  
 625 630 635 640

Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr  
 645 650 655

Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro  
 660 665 670

Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro  
 675 680 685

Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro  
 690 695 700

Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly  
 705 710 715

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

TATATAAAGC TTGCCGCCAC CATGGGCCAC ACACGGAGGC AG

42

10 (2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

25 ACTCCACCAG CTTACCTCG TTATCAGGAA AATGCTCTTG CTTGG

45

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

AGAGCATT TTT CCTGATAACG AGGTGAAGCT GGTGGAGTCT GGAGG

45

5

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129;

20

CCAGGCATCC CAGGGTCACC ATGGAGTTAG TTTGGGCAGC

40

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

30

(ii) MOLECULE TYPE: other nucleic acid

(ix) **FEATURE:**

(A) NAME/KEY: CDS

(B) LOCATION: 16..1435

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AAGCTTGCCG CCACC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 51

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser

5                          1                          5                          10

AAG TGT CCA TAC CTC AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 99

Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu

**15**                      **20**                      **25**

10

TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 147

Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu

**30                      35                      40**

15 GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA 195

Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala

**45                      50                      55                      60**

CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG 243

20 Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met

**65**                                      **70**                                      **75**

ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC 291

Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile

25                      80                      85                      90

TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA 339

Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro

**95                      100                      105**

30

TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC 387

Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp

110                      115                      120

35 GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT 435

Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala

125                      130                      135                      140

[illegible]

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	GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT	483
	Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn	
	145 150 155	
5	ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC	531
	Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His	
	160 165 170	
	CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA	579
10	Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr	
	175 180 185	
	GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG	627
	Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu	
15	190 195 200	
	GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT	675
	Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr	
	205 210 215 220	
20	GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA	723
	Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln	
	225 230 235	
25	GAG CAT TTT CCT GAT AAC GAG GTG AAG CTG GTG GAG TCT GGA GGA GGC	771
	Glu His Phe Pro Asp Asn Glu Val Lys Leu Val Glu Ser Gly Gly Gly	
	240 245 250	
30	TTG GTA CAG CCT GGG GGT TCT CTG AGA CTC TCC TGT GCA ACT TCT GGG	819
	Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly	
	255 260 265	
	TTC ACC TTC ACT GAT TAC TAC ATG AAC TGG GTC CGC CAG CCT CCA GGA	867
35	Phe Thr Phe Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly	
	270 275 280	
	AAG GCA CTT GAG TGG TTG GGT TTT ATT GGA AAC AAA GCT AAT GGT TAC	915

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Lys Ala Leu Glu Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr  
285                      290                      295                      300

ACA ACA GAG TAC AGT GCA TCT GTG AAG GGT CGG TTC ACC ATC TCC AGA 963  
5 Thr Thr Glu Tyr Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg  
305 310 315

GAC AAA TCC CAA AGC ATC CTC TAT CTT CAA ATG AAC ACC CTG AGA GCT 1011  
 Asp Lys Ser Gln Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala  
 10 320 325 330

GAG GAC AGT GCC ACT TAT TAC TGT ACA AGA GAT AGG GGG CTA CGG TTC 1059  
Glu Asp Ser Ala Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe  
335 340 345

TAC TTT GAC TAC TGG GGC CAA GGC ACC ACT CTC ACA GTC TCC TCA GCC 1107  
Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala  
350 355 360

20 AAA ACG ACA CCC CCA TCT GTC TAT CCA CTG GCC CCT GGA TCT GCT GCC 1155  
Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala  
365 370 375 380

CAA ACT AAC TCC ATG GTG ACC CTG GGA TGC CTG GTC AAG GGC TAT TTC 1203  
25 Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe  
385 390 395

30 CCT GAG CCA GTG ACA GTG ACC TGG AAC TCT GGA TCT CTG TCC AGC GGT 1251  
Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly  
400 405 410

GTG	CAC	ACC	TTC	CCA	GCT	GTC	CTG	CAG	TCT	GAC	CTC	TAC	ACT	CTG	AGC	1299
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	
415				420				425								

AGC TCA GTG ACT GTC CCC TCC AGC ACC TGG CCC AGC GAG ACC GTC ACC 1347  
Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr  
430 435 440

[illegible]



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TGC AAC GTT GCC CAC CCG GCC AGC AGC ACC AAG GTG GAC AAG AAA ATT 1395  
 Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile  
 445 450 455 460

5

GTG CCC AGG GAT TGT GGT TGT AAG CCT TGC ATA TGT ACA T AGTAAGAATT 1445  
 Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr  
 465 470

10 c

1446

(2) INFORMATION FOR SEQ ID NO: 131:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr  
 1 5 10 15

25

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys  
 20 25 30

30

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu  
 35 40 45

Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile  
 50 55 60

35

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp  
 65 70 75 80

[illegible]

35 Gly Gly Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Thr  
260 265 270

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Asp Tyr Tyr Met Asn Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu  
275 280 285

5 Trp Leu Gly Phe Ile Gly Asn Lys Ala Asn Gly Tyr Thr Thr Glu Tyr  
290 295 300

Ser Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Gln  
305                      310                      315                      320

10 Ser Ile Leu Tyr Leu Gln Met Asn Thr Leu Arg Ala Glu Asp Ser Ala  
325 330 335

Thr Tyr Tyr Cys Thr Arg Asp Arg Gly Leu Arg Phe Tyr Phe Asp Tyr  
340 345 350

15  
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro  
 355 360 365

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser  
20 370 375 380

Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val  
385 390 395 400

25 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe  
405 410 415

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr  
420 425 430

30  
Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala  
435 440 445

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp  
35            450                    455                            460

Cys Gly Cys Lys Pro Cys Ile Cys Thr  
465 470

[illegible]